

AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Paragraph at page 5, lines 16-22:

Figures 1A-1B present Figure 1 presents an alignment of amino acid sequences of Glu-tRNA reductase encoded by the nucleotide sequences derived from corn clone csc1c.pk005.i15 (SEQ ID NO:4) and soybean clone sfl1.pk0060.c4 (SEQ ID NO:12), and the Glu-tRNA reductase from *Glycine max* (NCBI GI No. 4324495; SEQ ID NO:29). Amino acids which are conserved among all and at least two sequences with an amino acid at that position are indicated with an asterisk (*). Dashes are used by the program to maximize alignment of the sequences.

Paragraph at page 5, lines 23-27:

Figures 2A-2B present Figure 2 presents an alignment of amino acid sequences of GSA aminotransferase encoded by the nucleotide sequence derived from rice clone rI0n.pk0078.b9 (SEQ ID NO:26) and the GSA aminotransferase from *Hordeum vulgare* (NCBI GI No: 1170029; SEQ ID NO:30). Amino acids which are conserved between the two sequences are indicated with an asterisk (*). Dashes are used by the program to maximize alignment of the sequences.

Paragraph at page 10, line 8 to line 30:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) J. Mol. Biol. 215:403-410 Altschul et al. (1993) J. Mol. Biol. 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic

acid fragment comprising the primers. Accordingly, a “substantial portion” of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 23, line 24 to page 24, line 15:

cDNA clones encoding aminolevulinic acid biosynthetic enzyme were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) J. Mol. Biol. 215:403-410 Altshul et al. (1993) J. Mol. Biol. 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/) searches for similarity to sequences contained in the BLAST “nr” database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the “nr” database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the “nr” database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet.* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as “pLog” values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST “hit” represent homologous proteins.

Paragraph at page 26, lines 1-5:

Figures 1A-1B present Figure 1 presents an alignment of the amino acid sequences set forth in SEQ ID NOs:4 and 12 and the *Glycine max* sequence (NCBI GI No. 4324495; SEQ ID NO:29). The data in Table 5 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:4 and 12 and the *Glycine max* sequence (NCBI GI No. 4324495; SEQ ID NO:29).

Paragraph at page 27, lines 28-32:

Figures 2A-2B present ~~Figure 2 presents~~ an alignment of the amino acid sequence set forth in SEQ ID NO:26 and the *Hordeum vulgare* sequence (NCBI GI No. 1170029; SEQ ID NO:30). The data in Table 8 represents a calculation of the percent identity of the amino acid sequence set forth in SEQ ID NO:26 and the *Hordeum vulgare* sequence (NCBI GI No. 1170029; SEQ ID NO:30).